

SPECIFICATION AMENDMENTS

The paragraph on page 59, line 19 to page 60, line 13 has been amended as follows

The ORF of the MN cDNA shown in Figures 1A-1C have the coding capacity for a 459 amino acid protein with a calculated molecular weight of 49.7 kd. MN protein has an estimated pI of about 4. As assessed by amino acid sequence analysis, the deduced primary structure of the MN protein can be divided into four distinct regions. The initial hydrophobic region of 37 amino acids (AA) corresponds to a signal peptide. The mature protein has an N-terminal part of 377 AA, a hydrophobic transmembrane segment of 20 AA and a C-terminal region of 25 AA. Alternatively, the MN protein can be viewed as having five domains as follows: (1) a signal peptide [amino acids (AA) 1-37; SEQ. ID. NO.: 6]; (2) a region of homology to collagen alpha1 chain (AA 38-135; SEQ. ID. NO.: 50); (3) a carbonic anhydrase domain (AA 136-391; SEQ. ID. NO.: 51); (4) a transmembrane region (AA ~~414-433~~ 415-434; SEQ. ID. NO.: 52); and (5) an intracellular C terminus (AA 435-459; SEQ. ID. NO.: 53). (The AA numbers are keyed to Figures 1A-1C.)

The information for SEQ ID NO: 28 in Sequence Listing has been amended as follows

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2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 1st MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ACACTCACCC CCATGGCTCC CCTGTCCCCC AGCCCCCTGCC TCCCTCTGTT GATCCCCCCC 60  
CCTGCTCCAG CCCTCACTGT CCAAATGCTG CTGTCACTGC TCCTTCTGCT GCCTCTCCAT 120  
CCCCAGAGGT TCCCCCGAT CCAGGAGGAT TCCCCCTTGC GAGGAGGCTC TTCTGGGAA 180  
GATGAECCAC TGGGGGAGGA CCATCTGCC AGTGAAGAGG ATTCAACCCAC ACAGGAGGAT 240  
CCACCEGGAG ACCAGGATCT ACCTGGACAC GACCATCTAC CTGGAGAGGA GGATCTACCT 300  
GAACTTAACC CTAAATCAGA ACAAGAGGGC TCCCTGAACT TAGAGGATCT ACCTACTGTT 360  
GAGGCTCCTG CAGATCCTCA AGAACCCCCAATAATCCCC ACAGGGACAA AGAAC 415  
  
GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCC 60  
AGCCCCCTGGC TCCCTCTGTT GATCCCAGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120  
CTGTCACTGC TGCTTCTGGT GCCTGTCCAT CCCAGAGGT TGCCCCGGAT GCAGGAGGAT 180  
TCCCCCTGG GAGGAGGCTC TTCTGGGAA GATGACCCAC TGGCGAGGA GGATCTGCC 240  
AGTGAAGAGG ATTCAACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300  
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAAGTTAACG CTAAATCAGA AGAAGAGGGC 360

TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420

AATAATGCCC ACAGGGACAA AGAAG 445

The information for SEQ ID NO: 52 in the Sequence Listing has  
been amended as follows

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: transmembrane region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

~~Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val~~  
~~1 5 10 15~~

~~Ala Phe Leu Val~~  
~~20~~

Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala  
1 5 10 15

Phe Leu Val Gln  
20